plates and is easily automated. It will fail only in the few cases were 5′-RNNNNY-3′ in strand (b) contains 5′-GACGC-3′, which is the recognition site for *Hga I*. The number of prior extension reactions required can be reduced by synthesis of more restricted pools of sequences. For example, using 4 pools where the base in one particular position is known in advance, such as 5′-YNNANR-3′.

Please replace the paragraph on page 57, lines 10-12 with the following:

To make the probes needed for positional SBH (as shown in FIG. 2A), the duplex PCR products are first attached to a solid support through streptavidin. They are then cleaved with *Bst XI* to generate the following pairs of products:

IN THE CLAIMS:

Please cancel claims 125 and 126 without prejudice or disclaimer.

Please add the following claims:

127. (New) An array of nucleic acid probes, wherein each probe comprises a single-stranded portion at one terminus, a double-stranded portion at the opposite terminus, and a random nucleotide sequence within the single-stranded portion, wherein

within the single-stranded portion of each probe, one base is used at a defined number of positions and all other bases except that base are in the remaining positions, and

the probes are fixed to a solid support by conjugating to a coupling agent.

128. (New) The array of claim 127, wherein the coupling agent is selected from the group consisting of antibody/antigen, biotin/streptavidin, *Staphylococcus aureus* protein A/IgG antibody F_c fragment, nucleic acid/nucleic acid binding protein, and streptavidin/protein A chimeras.

129. (New) The array of claim 127, wherein the probes are labelled with a detectable label.

130. (New) The array of claim 129, wherein the detectable label is selected from the group consisting of a radioisotope, a stable isotope, an enzyme, an antibody, a fluorescent chemical, a luminescent chemical, a chromatic chemical, and a metal.

131. (New) The array of claim 127, wherein the nucleic acids are DNA, RNA, Protein Nucleic Acid (PNA), or a combination thereof.

132. (New) The array of claim 127, wherein the solid support is selected from the group consisting of plastics, ceramics, metals, resins, gels, membranes, and chips.

133. (New) The array of claim 127, wherein the solid support is a two-dimensional or a three-dimensional matrix with multiple probe binding sites.

134. (New) The array of claim 74, wherein the random nucleotide sequence includes a gapped segment.

135. (New) The array of claim 74, wherein the nucleic acid comprises at least one modified base.

Please replace claims 70, 73 and 74 with amended claims 70, 73 and 74 as follows:

70. (Twice Amended) An array of nucleic acid probes, wherein

each probe has a double-stranded portion at the 3'-terminus, a degenerate single-stranded portion at the 5'-terminus, and a random nucleotide sequence of length R within the single-stranded portion.

73. (Amended) The array of claim 70, wherein the probes are fixed to a solid support by conjugating to a coupling agent selected from the group consisting of antibody/antigen, biotin/streptavidin, *Staphylococcus aureus* protein A/IgG antibody F_c fragment, nucleic acid/nucleic acid binding protein, and streptavidin/protein A chimeras.

74. (Amended) An array of nucleic acid probes, wherein each probe comprises a single-stranded portion at one terminus and a double-stranded portion at the opposite terminus, wherein

the single-stranded portion includes a random nucleotide sequence of length R, and an adjacent sequence of nucleotides comprising ligated nucleic acid present in a target nucleic acid; and

one strand of the double-stranded portion is conjugated to a coupling agent through which the probes are fixed to a solid support.